

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2005, 13:26:44 ; Search time 39 Seconds
(without alignments)
286.183 Million cell updates/sec

Title: US-10-659-782A-32

Perfect score: 616
Sequence: 1 MPSPGTVCSLLGLMLDL.....PPSRRRSRHQPSCPSEL 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description |
|------------|-------|-------|--------|-----------|--------------------|
| 1 | 198 | 32.1 | 117 | 1 A59316 | ghrelin precursor |
| 2 | 159.5 | 25.9 | 117 | 1 B59316 | ghrelin precursor |
| 3 | 75.5 | 12.3 | 573 | 2 JC4335 | anti-mullerian hor |
| 4 | 72.5 | 11.8 | 519 | 2 G84707 | probable MYB famil |
| 5 | 72.5 | 11.8 | 666 | 2 T22943 | hypothetical prote |
| 6 | 72.5 | 11.8 | 725 | 1 E64211 | virulence-associat |
| 7 | 72 | 11.7 | 764 | 2 I48882 | thyrotropin recept |
| 8 | 70 | 11.4 | 307 | 2 T33503 | hypothetical prote |
| 9 | 69.5 | 11.3 | 302 | 2 H96792 | unknown protein F1 |
| 10 | 68.5 | 11.1 | 449 | 2 C39926 | hypothetical 51.8K |
| 11 | 68.5 | 11.1 | 456 | 2 T35474 | 50kD proline rich |
| 12 | 68.5 | 11.1 | 796 | 2 T32425 | hypothetical prote |
| 13 | 68 | 11.0 | 94 | 2 B75564 | hypothetical prote |
| 14 | 68 | 11.0 | 764 | 2 A35956 | thyrotropin recept |
| 15 | 67.5 | 11.0 | 136 | 2 AG0449 | regulator of nucle |
| 16 | 67.5 | 11.0 | 363 | 2 F91265 | sensor protein Bas |
| 17 | 67.5 | 11.0 | 363 | 2 C86106 | sensor protein for |
| 18 | 67.5 | 11.0 | 363 | 2 JX02857 | sensor protein bas |
| 19 | 67.5 | 11.0 | 406 | 2 T28957 | hypothetical prote |
| 20 | 67.5 | 11.0 | 1704 | 2 A59188 | ATP-binding casset |
| 21 | 67.5 | 11.0 | 1704 | 2 S71363 | probable ATP-bind |
| 22 | 67 | 10.9 | 267 | 2 AB0461 | probable carboxyme |
| 23 | 67 | 10.9 | 381 | 2 S16506 | hypothetical prote |
| 24 | 67 | 10.9 | 749 | 2 A75560 | conserved hypothet |
| 25 | 66.5 | 10.8 | 458 | 2 AC0216 | para-aminobenzoate |
| 26 | 66.5 | 10.8 | 540 | 2 T27400 | hypothetical prote |
| 27 | 66 | 10.7 | 944 | 2 T41711 | probable alpha-tre |
| 28 | 65.5 | 10.6 | 1037 | 2 B64187 | conserved hypothet |
| 29 | 65 | 10.6 | 309 | 2 S77905 | lyase - Pseudomona |

ALIGNMENTS

RESULT 1

A59316
ghrelin precursor - human
N;Alternate names: preproghrelin
C:Species: Homo sapiens (man)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59316
R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A;Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: A59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-117 <KOJ>
A:Cross-references: UNIPROT:Q9UBU3; GB:AB029434; NID:g6691571; PIDN:BAA89371.1; PID:g66
A:Experimental source: tissue stomach endocrine cells
A;Note: submitted to GenBank, June 1999
C;Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (grow
C;Superfamily: motilin
C;Keywords: hormone; lipoprotein; stomach
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-51/Product: ghrelin #status predicted <MAT>
F;52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 32.1%; Score 198; DB 1; Length 117;
Best Local Similarity 88.6%; Pred. No. 1.6e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MPSPGTVCSLLGLMLDLAMAGSSFLSPHQVQVRPPHKAP 44
DB 1 MPSPGTVCSLLGLMLDLAMAGSSFLSPHQVQVRPPHKAP 44

RESULT 2

B59316
ghrelin precursor - rat
N;Alternate names: preproghrelin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
C:Accession: B59316
R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A;Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: B59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA; protein
A;Residues: 1-117 <KOJ>
A:Cross-references: UNIPROT:Q9QYH7; GB:AB029433; NID:g6691569; PIDN:BAA89370.1; PID:g66
A:Experimental source: strain SD; tissue stomach endocrine cells

30 65 10.6 383 2 A56084 interleukin-lbета
31 65 10.6 490 2 S67581 STP4 protein - yea
32 64.5 10.5 187 2 T51876 hypothetical prote
33 64.5 10.5 354 2 G75548 ABC transporter, A
34 64.5 10.5 467 1 S45493 serine proteinase
35 64.5 10.5 594 2 T15202 hypothetical prote
36 64.5 10.5 761 2 T15776 hypothetical prote
37 64.5 10.5 1001 2 T28897 hypothetical prote
38 64.5 10.5 1487 2 S62048 probable membrane
39 64.5 10.5 6805 2 S20901 titin - rabbit (fr
40 64 10.4 413 2 E82312 phase integrase VC
41 64 10.4 555 2 H83043 hypothetical prote
42 64 10.4 637 2 T03842 fission yeast skbl
43 63.5 10.3 122 2 AG3144 hypothetical prote
44 63.5 10.3 428 2 JH0634 site-specific DNA-
45 63.5 10.3 522 2 S33029 hypothetical prote

A;Note: submitted to GenBank, June 1999
 C;Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth)
 C;Superfamily: motilin
 C;Keywords: hormone; lipoprotein; stomach
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-51/Product: ghrelin #status predicted <MAT>
 F;52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F;26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 25.9%; Score 159.5; DB 1; Length 117;
 Best Local Similarity 40.0%; Pred. No. 1.7e-09;
 Matches 42; Conservative 7; Mismatches 33; Indels 23; Gaps 2;

QY 1 MPSPGVTCVLLGLMLDLAMAGSFLSPHQVRPPKAPHVVPALPLSNQLCDLE 60
 DB 1 MVSSATICSLLLSMLMDMAMAGSFLSPHQVRPPKAPHVVPALPLSNQLCDLE 54

QY 61 QQRH-----WASVFSQSTKDSGDLTVSGRTWG 88
 DB 55 GWLHPEDRGQAEEAELEIRFNAPFDVGIKLSGAQYQHQGRALG 99

RESULT 3
 JC4335
 anti-mullerian hormone type II receptor precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 06-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 16-Aug-2004
 C;Accession: JC4335
 R;Visser, J.A.; McLuskey, A.; van Beers, T.; Weghuis, D.O.; van Kessel, A.G.; Grootegeed
 Biochem. Biophys. Res. Commun. 215, 1029-1036, 1995
 A;Title: Structure and chromosomal localization of the human anti-mullerian hormone type
 A;Reference number: JC4335; MUID:96028015; PMID:7488027
 A;Accession: JC4335
 A;Molecule type: mRNA
 A;Residues: 1-573 <VIS>
 A;Cross-references: UNIPROT:Q16671; GB:X91156; NID:g1107671; PIDN:CAA62593.1; PID:e19804
 C;Comment: This is a receptor for anti-mullerian hormone (see PIR:WFHUM). It plays a cri
 C;Genetics:
 A;Gene: GDB:AMHR2
 A;Cross-references: GDB:696210; OMIM:600956
 A;Map position: 12q13-12q13
 C;Introns: 16/3; 77/3; 141/3; 167/3; 207/2; 284/2; 322/3; 380/2; 429/3; 475/2
 C;Superfamily: protein kinase homology
 C;Keywords: ATP; hormone receptor; transmembrane protein
 F;1-16/Domain: signal sequence #status predicted <SIG>
 F;17-573/Product: anti-mullerian hormone type II receptor #status predicted <MAT>
 F;17-141/Domain: extracellular hormone binding #status predicted <ELB>
 F;142-167/Domain: transmembrane #status predicted <TM>
 F;201-512/Domain: protein kinase homology <KIN>

Query Match 12.3%; Score 75.5; DB 2; Length 573;
 Best Local Similarity 28.7%; Pred. No. 5.7;
 Matches 33; Conservative 15; Mismatches 44; Indels 23; Gaps 3;

QY 3 SPGTVC-----LLLLMLDLAMAGS---SFLSPHQVRPPKAPH 45
 DB 128 SPGTGSGQQAQGESIWMALVLLGLLLLVLSIILALQKNYVRGEP----- 181

QY 46 VVPALPLSNQLCDLEQQRHWSVFSQSTKDSGDLTVSGRTWGLVNLRLFPSS 100
 DB 182 VPEPRPDSGRDWSVELQELPELCPFSQVIREGGHAVVWAGOLQGLVAIKAFPPRS 236

RESULT 4
 G84707
 probable MYB family transcription factor [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: G84707
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: G84707
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-519 <STO>
 A;Cross-references: UNIPROT:Q8RYE3; GB:AE002093; NID:96598822; PIDN:AAB63073.2; GSPDB:GN0023;
 C;Genetics:
 A;Gene: At2g30380
 A;Map position: 2

Query Match 11.8%; Score 72.5; DB 2; Length 519;
 Best Local Similarity 26.9%; Pred. No. 10;
 Matches 21; Conservative 13; Mismatches 27; Indels 17; Gaps 5;

QY 17 WDLAMAGSFLSPHQVRP---PHKAPHVVPALPLSNQL---CDLEQQRHW-ASVF 69
 DB 431 WYDL-VTGKILALDLHTEQFDVPRPHGSPTLAPLANLEDLAMICDYEFSHWKVAIW 489

QY 70 SQSTKDSGDLTVSGRTW 87
 DB 490 TMDTQ-----ETW 498

RESULT 5
 T22943
 hypothetical protein F58G11.3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T22943
 R;Percy, C.
 submitted to the EMBL Data Library, October 1996
 A;Reference number: Z19640
 A;Accession: T22943
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-666 <WIL>
 A;Cross-references: UNIPROT:P90898; EMBL:Z81094; PIDN:CA803154.1; GSPDB:GN00023; CESP:FP5
 C;Experimental source: clone F58G11
 C;Genetics:
 A;Gene: CESP:F58G11.3
 A;Map position: 5
 A;Introns: 42/2; 82/2; 153/3; 274/3; 380/1; 569/3; 613/3

Query Match 11.8%; Score 72.5; DB 2; Length 666;
 Best Local Similarity 26.9%; Pred. No. 14;
 Matches 32; Conservative 10; Mismatches 42; Indels 35; Gaps 5;

QY 33 QRQVRPPHKAPHVVPALPLSNQLCDLEQQRHWA--SVFSQSTKDSGSD----- 79
 DB 537 QRVRVNPQCVKVVVPTLGOALAEVRQRQEQVEAFNEQPEPSPRLGMGSSSHAA 596

QY 80 LTVSGRTWGLVNLN-----LFPSS-----RERSR-----RSHQPSCSPEL 116
 DB 597 SNVSDGGAQVQVQKVEKSPRPFTVLLPPMKGAGVKIRPSRVVLCHSSASSFPFSL 655

RESULT 6
 E84211
 virulence-associated protein vacB homolog - Mycoplasma genitalium
 C;Species: Mycoplasma genitalium
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: E84211
 R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
 M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.;
 C.; Venter, J.C.
 Science 270, 397-403, 1995
 A;Title: The minimal gene complement of Mycoplasma genitalium.
 A;Reference number: A84200; MUID:96026346; PMID:7569993
 A;Accession: E84211
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-725 <TIGR>

A;Cross-references: UNIPROT:P47350; GB:U93690; GB:L43367; NID:g1045782; PID:g1045783; T

C;Experimental source: strain G-37

C;Genetics:

A;Genetic code: SGC3

C;Superfamily: virulence-associated protein vacB homolog

Query Match 11.8%; Score 72.5; DB 1; Length 725;
Best Local Similarity 26.7%; Pred.No.15;
Matches 27; Conservative 16; Mismatches 37; Indels 21; Gaps 4;

Qy 18 LDLAGAGSFLSPHQVVRPPHAP-----HVVPALP--LSNOLCDLE-QQRHWAS 67
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 298 LYVAIDAVHYVNRSIDIEAKHTSSIVLPGHYVFMPLPEQLSNOLCSLNPAQKRYVV 357
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Qy 68 VFSQSTKDSGLTVSGRTWGLRVNLRLFPSPSRERSRSH 108
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 358 VCEISFDNQRIKT-----NKLYPATIISKRFYSY 387
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 7

I48882

N;thyrotropin receptor precursor - mouse

N;Alternate names: thyroid-stimulating hormone receptor; TSH receptor

C;Species: Mus musculus (house mouse)

C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004

C;Accession: I48882

R;Stein, S.A.; Oates, E.L.; Hall, C.R.; Grumblies, R.M.; Fernandez, L.M.; Taylor, N.A.; H

Mol. Endocrinol. 8, 129-138, 1994

A;Title: Identification of a point mutation in the thyrotropin receptor of the hyc/hyt h

A;Reference number: A54271; MOID:94224232; PMID:8170469

A;Accession: I48882

A;Status: preliminary

A:Molecule type: mRNA

A;Residues: 1-764 <RES>

A;Cross-references: UNIPROT:P47750; EMBL:U02602; NID:g575923; PIDN:AAB60455.1; PID:g5759

C;Genetics:

A;Gene: TSHR

C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat h

C;Keywords: G protein-coupled receptor; transmembrane protein

F;53-76/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F;77-101/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F;102-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F;127-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F;152-176/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F;179-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F;201-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

Query Match 11.7%; Score 72; DB 2; Length 764;
Best Local Similarity 29.5%; Pred.No.18;
Matches 33; Conservative 15; Mismatches 48; Indels 16; Gaps 5;

Qy 4 PGTVCSEILLGMLWLDMAGSSFPSPE---HQEVQVRPHKAPHVVPALPLSNOLCDLE 60
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 3 PGSL--LLLVLILALSRLSKKECAPPCBCHQEDDFRVTCRELHRIPSPPTQTLLKL- 59
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Qy 61 QQRHWASV----FSQSTKDSGLTVSGRTWGLRVNLRLFPSPSRERSRSH 108
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 60 IETHLKTIPLAFSSSLNIRIYLSDA-----TLQRLPHSFYNLSRWTH 105
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 8

T33503

hypothetical protein C50E10.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T33503

R;Nelson, J.; Klinke, B.; Wohlgmann, P.; Bauer, C.

submitted to the EMBL Data Library, October 1998

A;Description: The sequence of C. elegans cosmid C50E10.

A;Reference number: Z21359

A;Accession: T33503

A;Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

[illegible]

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